



SEQUENCE LISTING

<120> THE SCRIPPS RESEARCH INSTITUTE
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GOTTESFELD, Joel M.
WRIGHT, Peter E.

F9
<120> ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR

<130> SCRIP1160-4

<140> US 09/500,700
<141> 2000-02-09

<150> US 08/863,813
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<150> US 08/676,318
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<151> 1995-01-18

<150> US 08/312,604
<151> 1994-09-28

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<170> PatentIn version 3.1

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Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa
1          5           10          15

Xaa Leu Xaa Xaa His Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa
20          25           30
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<213> Artificial Sequence

<220>
<223> Primer for amplification of pZif89

<400> 2
atgaaaactgc tcgagcccta tgcttgccct gtcgag 36

<210> 3
<211> 45
<212> DNA
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<220>
<223> Primer for amplification of pZif89

<400> 3
gaggaggagg agactagtgt ccttctgtct taaatggatt ttggc 45

<210> 4
<211> 273
<212> DNA
<213> Mouse

<220>
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<222> (1)..(273)
<223>

<400> 4
ctc gag ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc ttt tct 48
Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
1 5 10 15

cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc cag aag 96
Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys
20 25 30

ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt gac cac 144
Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His
35 40 45

ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt gcc tgt 192
Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
50 55 60

gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag agg cat 240
Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His
65 70 75 80

acc aaa atc cat tta aga cag aag gac act agt
Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser 273
85 90

<210> 5

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<211> 91
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<213> Mouse

<400> 5

Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
1 5 10 15

Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys
20 25 30

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His
35 40 45

Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
50 55 60

Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His
65 70 75 80

Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser
85 90

<210> 6
<211> 22
<212> DNA
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<223> FTX3 primer

<400> 6
gcaattaacc ctcactaaag gg 22

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> BZF3 primer

<400> 7
ggcaaacttc ctccccacaaa t 21

<210> 8
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<212> DNA
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<223> ZF36K primer

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atttgtggga ggaagtttgc cnnkagtnnk nnknnknnkn nkcataccaa aatccattta      60

<210> 9
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<212> DNA
<213> Artificial Sequence

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<223> R3B primer

<400> 9
ttgatattca caaacgaatg g                                21

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> ZFNsiB primer

<400> 10
catgcatatt cgacactgga a                                21

<210> 11
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<212> DNA
<213> Artificial Sequence

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<223> ZF2r6F primer

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<221> misc_feature
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cagtgtcgaa tatgcatgct taacttcnnk nnknnknnkn nknnkaccac ccacatccgc      60
acccac                                         66

<210> 12
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<223> ZFI6rb primer

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ctggcctgtg tggatgcgga tatgmnnmnn mnnmnnmnnnc gamnnagaaa agcggcgatc      60
gcagga                                         66

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> ZF1F primer

<400> 13
catatccgca tccacacagg ccag                                         24

<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified sequence of finger 1 of zif268

<400> 14
Arg Ser Asp Glu Leu Thr Arg His
1                      5

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified sequence of finger 2 of zif268

<400> 15
Ser Arg Ser Asp His Leu
1                      5

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

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<223> Hairpin oligonucleotide of a phage library containing phages

<400> 16
cgtaaatggg cgccctttg ggcgcccatt tacg                                         34

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<210> 17
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<220>
<223> Binding sequence of zif268 finger 3

<400> 17

Arg Ser Asp Glu Arg Lys Arg His
1 5

<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Binding sequence of zif268 finger 3

<400> 18

Trp Ser Ile Pro Val Leu Leu His
1 5

<210> 19
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Binding sequence of zif268 finger 3

<400> 19

Trp Ser Leu Leu Pro Val Leu His
1 5

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Binding sequence of zif268 finger 3

<400> 20

Phe Ser Phe Leu Leu Pro Leu His
1 5

<210> 21
<211> 8
<212> PRT

<213> Artificial Sequence

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<223> Binding sequence of zif268 finger 3

<400> 21

Leu Ser Thr Trp Arg Gly Trp His
1 5

<210> 22

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 22

Thr Ser Ile Gln Leu Pro Tyr His
1 5

<210> 23

<211> 61

<212> DNA

<213> Homo sapiens

<400> 23

tgatctcaga agccaagcag ggtcgccct ggttagtact tggatggag accgcctggg 60

a

61

<210> 24

<211> 26

<212> PRT

<213> Homo sapiens

<400> 24

Tyr Ile Cys Ser Phe Ala Asp Cys Gly Ala Ala Tyr Asn Lys Asn Trp
1 5 10 15

Lys Leu Gln Ala His Leu Cys Lys His Thr
20 25

<210> 25

<211> 26

<212> PRT

<213> Homo sapiens

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Phe Pro Cys Lys Glu Glu Gly Cys Glu Lys Gly Phe Thr Ser Leu His
1 5 10 15

His Leu Thr Arg His Ser Leu Thr His Thr
20 25

<210> 26
<211> 26
<212> PRT
<213> Homo sapiens

<400> 26

Phe Thr Cys Asp Ser Asp Gly Cys Asp Leu Arg Phe Thr Thr Lys Ala
1 5 10 15

Asn Met Lys Lys His Phe Asn Arg Phe His
20 25

<210> 27
<211> 13
<212> DNA
<213> Homo sapiens

<400> 27
tggatggag acc 13

<210> 28
<211> 25
<212> PRT
<213> Mouse

<400> 28

Arg Gln Lys Asp Ser Arg Thr Ser Thr Ser Gly Gln Ala Gly Gln Tyr
1 5 10 15

Pro Tyr Asp Val Pro Asp Tyr Ala Ser
20 25

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification of fragments of zif268

<400> 29
gtccataaga ttagcggatc c 21

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer for amplification of fragments of zif268

<400> 30
 gtgagcgagg aagcggaga g

21

<210> 31
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 <212> DNA
 <213> Artificial Sequence

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<400> 31
 cctgcgtggg cgccctttg ggcccccacg cagg

34

<210> 32
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Thr Gly Glu Xaa
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 <211> 462
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 <213> Mouse

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 Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
 1 5 10 15

48

ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30

96

cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45

144

gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt	192
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe	
50 55 60	
gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag	240
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys	
65 70 75 80	
agg cat acc aaa atc cat acc ggt cag aag ccc act agt ggc ggt ggt	288
Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly	
85 90 95	
cgg atc gcc cggt ctg gag gaa aaa gtg aaa acc ttg aaa gcg caa aac	336
Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn	
100 105 110	
tcc gag ctg gcg tcc acc gcc aac atg ctc agg gaa cag gtg gca cag	384
Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln	
115 120 125	
ctt aaa cag aaa gtc atg aac cac gct agc ggc cag ggc cag tac	432
Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr	
130 135 140	
ccg tac gac gtt ccg gac tac gct tct taa	462
Pro Tyr Asp Val Pro Asp Tyr Ala Ser	
145 150	
<210> 34	
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<400> 34	
Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg	
1 5 10 15	
Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly	
20 25 30	
Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser	
35 40 45	
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe	
50 55 60	
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys	
65 70 75 80	
Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly	
85 90 95	
Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn	

100 105 110

Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln
115 120 125

Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr
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Pro Tyr Asp Val Pro Asp Tyr Ala Ser
145 150

<210> 35
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1          5           '          10          15

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ttt tct cgc tcg gag ctt acc cgc cat atc cgc atc cac aca ggc
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30

cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt 144
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45

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gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt      192
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
      50          55          60

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gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag      240
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
65           70           75           80

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agg cat acc aaa atc cat acc ggt cag aag ccc act agt ggc ggt ggt
 Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly
 85 90 95

ctg acc gac acc ctg cag gcg gaa acc gac cag ctg gaa gac gaa aaa
 Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
 100 105 110

tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag 384
 Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
 115 120 125

ctg gag ttc atc ctg gcg gca cac gct agc ggc cag gcc ggc cag tac 432
 Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr
 130 135 140

ccg tac gac gtt ccg gac tac gct tct taa 462
Pro Tyr Asp Val Pro Asp Tyr Ala Ser
145 150

<210> 36
<211> 153
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<400> 36

Met	Leu	Glu	Leu	Pro	Tyr	Ala	Cys	Pro	Val	Glu	Ser	Cys	Asp	Arg	Arg
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Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
20 25 30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
35 40 45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
50 55 60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
65 70 75 80

Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly
85 90 95

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
100 105 110

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
115 120 125

Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr
130 135 140

Pro Tyr Asp Val Pro Asp Tyr Ala Ser
145 150

<210> 37

<213> DNA
<213> Artificial Sequence

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<223> Single stranded low

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<222> (10)..(10)
<223> n is any nucleotide. n can be any number of nucleotides
<400> 37
cgcccacgcn gcgtggcgcg

19

<210> 38
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<213> Artificial Sequence
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<223> Single-stranded leucine zipper domain of zif268-Fos
<220>
<221> misc_feature
<222> (10)..(10)
<223> n is any nucleotide. n can be any number of nucleotides
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cgcccacgcn gcggcggcgg cggcggcgcg

28

<210> 39
<211> 67
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<223> Construction of C7 zinc finger
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<222> (67)..(67)
<223> Xaa is Tyr-Ala-Cys-Pro-Val-Glu-Ser-Cys-Asp-Arg-Arg-Phe-Ser-Lys-
-Ser-Ala-Asp-Leu-Lys-Arg-His-Ile-Arg-Ile-His-Thr-Gly-Glu-Lys-Pro
could be repeated 10 times
<400> 39

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr
20 25 30

Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe
35 40 45

Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu
50 55 60

Lys Pro Xaa
65

<210> 40
 <211> 34
 <212> DNA
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<210> 41
 <211> 294
 <212> DNA
 <213> Homo sapiens

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 <222> (1)..(294)
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 1 5 10 15

cgc ttt tct aag tcg gct gat ctg aag cgc cat atc cgc atc cac act 96
 Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr
 20 25 30

ggc gaa aaa ccg tac gcg tgc cct gtc gag tcc tgc gat cgc cgc ttt 144
 Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe
 35 40 45

tct aag tcg gct gat ctg aag cgc cat atc cgc atc cac acc ggg gag 192
 Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu
 50 55 60

aag ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc ttt tct aag 240
 Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys
 65 70 75 80

tcg gct gat ctg aag cgc cat atc cgc atc cac acc ggt cag aag ccc 288
 Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
 85 90 95

act agt 294
 Thr Ser

<210> 42
 <211> 98
 <212> PRT
 <213> Homo sapiens

 <400> 42

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
 1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr
 20 25 30

Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe
 35 40 45

Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu
 50 55 60

Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys
 65 70 75 80

Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
 85 90 95

Thr Ser

<210> 43
<211> 543
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> CDS
<222> (1)..(543)
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1 5 10 15

ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc 96
Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
20 25 30

cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt 144
Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
35 40 45

gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt 192
Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
50 55 60

gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag 240
Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
65 70 75 80

agg cat acc aaa atc cat acc ggg gag aag ccc tat gct tgc cct gtc Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val 85 90 95	288
gag tcc tgc gat cgc cgc ttt tct cgc tcg gat gag ctt acc cgc cat Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His 100 105 110	336
atc cgc atc cac aca ggc cag aag ccc ttc cag tgt cga ata tcc atg Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met 115 120 125	384
cgt aac ttc agt cgt agt gac cac ctt acc acc cac atc cgc acc cac Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His 130 135 140	432
aca ggc gag aag cct ttt gcc tgt gac att tgt ggg agg aag ttt gcc Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala 145 150 155 160	480
agg agt gat gaa cgc aag agg cat acc aaa atc cat tta aga cag aag Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys 165 170 175	528
gac tct aga act agt Asp Ser Arg Thr Ser 180	543

<210> 44
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<213> Artificial Sequence

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<223> zif268-zif268 with TGEKP linker
<400> 44

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
1 5 10 15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
20 25 30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
35 40 45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
50 55 60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
65 70 75 80

Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val

85

90

95

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His
 100 105 110

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met
 115 120 125

Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
 130 135 140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
 145 150 155 160

Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
 165 170 175

Asp Ser Arg Thr Ser
 180

<210> 45
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for generation of 5' C7

<400> 45
gaggaggagg agggatccat gctcgagctc ccctatgctt gccctg 46

<210> 46
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for generation of 5' C7

<400> 46
gaggaggaga ccgttatgga ttttggtatg cctcttgcg 39

<210> 47
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for generation of 3' C7

<400> 47
gaggaggaga ccgttgagaa gcccstatgct tgccctgtcg agtcctgcga tcgcccc 57

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<210> 48
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for generation of 3' C7

<400> 48
gaggaggaga ctagttctag agtccttctg tc          32

<210> 49
<211> 38
<212> DNA
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<220>
<223> Primary strand within a duplex region of a probe for C7-C7 site

<400> 49
gatgtatgta gcgtgggcgg cgtggcgta agtaatgc      38

<210> 50
<211> 38
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<220>
<223> Primary strand within a duplex region of a probe for SP1C-C7 site

<400> 50
gatgtatgta gcgtgggcgg gggcggggtta agtaatgc      38

<210> 51
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primary strand within a duplex region of a probe for (GCG)6 site

<400> 51
gatgtatgta gcggcggcgg cggcggcgta agtaatgc      38

<210> 52
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primary strand within a duplex region of a probe for C7 site

<400> 52
gatgtatgta gcgtggcgt aagtaatgc                  29

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<210> 53
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primary strand within a duplex region of a probe for Sp1C site

<400> 53
gatgtatgta gggcggggt aagtaatgc                                29

<210> 54
<211> 28
<212> PRT
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<220>
<223> Conserved portion of Zif268 protein

<400> 54

Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg
1           5           10          15

Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu
20          25

<210> 55
<211> 41
<212> DNA
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<220>
<223> EcoRIfootF primer

<400> 55
gaggaggagg aattccgaca tttataatga acgtgaattg c                                41

<210> 56
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> C7-C73>5 primer

<400> 56
tgcccccacg ccgccccacgc gatgattggg agctttttt gcacg                                45

<210> 57
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<212> DNA
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<220>

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<223> C7-C75>3 primer

<400> 57

tgcgtgggc ggcgtggcg caaaaaatta ttatcatgga ttctaaaacg g

51

<210> 58

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> NotIfootB primer

<400> 58

gaggaggagg cggccgcagg tagatgagat gtgacgaacg tg

42

<210> 59

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Sp1C-C73>5 primer

<400> 59

tgcggccccc ccgccccacgc gatgattggg agctttttt gcacg

45

<210> 60

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Sp1C75>3 primer

<400> 60

tgcgtgggc gggggcgggg caaaaaatta ttatcatgga ttctaaaacg g

51

<210> 61

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Target sequence of six finger protein C7-C7

<400> 61

gcgtggcgg cggtggcg

18

<210> 62

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Target sequence of six-finger protein Sp1C-C7

<400> 62	
gcgtggcg ggccgggg	18
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<223> Altered zif268 finger 1 binding site	
<400> 63	
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cctgcgttgg cgccctttg ggcgccaaacg cagg	34
<210> 65	
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<212> DNA	
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cctctgtggg cgccctttg ggcgcccaca gagg	34
<210> 66	
<211> 5	
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<223> Linker peptide	
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Thr Gly Gln Lys Pro	
1	5
<210> 67	
<211> 5	
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<223> Linker peptide

<400> 67

Thr Gly Glu Lys Pro
1 5

<210> 68

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> (GCG)6 probe

<400> 68

gcggcggcg 18
ggccggcg

<210> 69

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> SV40 large T antigen

<400> 69

Pro Lys Lys Arg Lys Val

1 5

<210> 70

<211> 28

<212> PRT

<213> Artificial Sequence

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<223> Conserved portion of Zif268 protein

<400> 70

Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg
1 5 10 15

Ser Asp His Leu Thr Thr His Ile Arg Thr His Thr
20 25

<210> 71

<211> 22

<212> DNA

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<223> Variant of zif268 sequence

<400> 71

tgcggccacg ccgccccacgc ga

22

<210> 72
<211> 22
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<400> 72
tgccccgccc ccgccccacgc ga

22

<210> 73
<211> 6
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<220>
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<400> 73

Arg Asp Glu Leu Thr Arg
1 5

<210> 74
<211> 6
<212> PRT
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<220>
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<400> 74

Lys Ala Asp Leu Lys Arg
1 5

<210> 75
<211> 6
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<220>
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<400> 75

Lys Cys Val Arg Gly Arg
1 5

<210> 76
<211> 6
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<220>

<223> Modified sequence of finger 1 of zif268

<400> 76

Lys Cys Asp Arg Gly Arg

1 5

<210> 77

<211> 6

<212> PRT

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<223> Modified sequence of finger 1 of zif268

<400> 77

Lys Tyr Cys Arg Thr Arg

1 5

<210> 78

<211> 6

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<223> Modified sequence of finger 1 of zif268

<400> 78

Lys Gln Leu Pro Trp Thr

1 5

<210> 79

<211> 6

<212> PRT

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<223> Modified sequence of finger 1 of zif268

<400> 79

Lys Asn Ser Gln His Pro

1 5

<210> 80

<211> 6

<212> PRT

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<220>

<223> Modified sequence of finger 1 of zif268

<400> 80

Lys Cys Gln Met Asp Ser
1 5

<210> 81
<211> 6
<212> PRT
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<220>
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<400> 81

Gln Gln Val Thr Arg Thr
1 5

<210> 82
<211> 6
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<220>
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<400> 82

Thr Gln Ser Gln Ser Pro
1 5

<210> 83
<211> 6
<212> PRT
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<220>
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<400> 83

Val His Ile Gln Ala Asn
1 5

<210> 84
<211> 6
<212> PRT
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<220>
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<400> 84

Gln Thr Ala Ser Lys Ala
1 5

<210> 85
<211> 6
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<220>
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<400> 85

Pro Thr His Leu Gln Thr
1 5

<210> 86
<211> 6
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<220>
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<400> 86

Pro Glu Arg Thr Gln Pro
1 5

<210> 87
<211> 6
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<400> 87

Thr Ser Glu Ala Asp His
1 5

<210> 88
<211> 6
<212> PRT
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<400> 88

Ser Glu Gln Arg Tyr Pro
1 5

<210> 89
<211> 6
<212> PRT
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<220>
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<400> 89

His Gln Gln Asn Lys Pro
1 5

<210> 90
<211> 6
<212> PRT
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<220>
<223> Modified sequence of finger 1 of zif268

<400> 90

Arg Gly Gln Gly Met Ala
1 5

<210> 91
<211> 6
<212> PRT
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<220>
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<400> 91

Arg Ala Arg Gln Thr Gly
1 5

<210> 92
<211> 6
<212> PRT
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<220>
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<400> 92

Glu Asn Ser Phe Thr Asp
1 5

<210> 93
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Modified sequence of finger 1 of zif268

<400> 93

Asn Val Met Gly His Asp
1 5

<210> 94
<211> 6
<212> PRT
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<220>
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<400> 94

Asn Arg Gly Gln Arg Lys
1 5

<210> 95
<211> 6
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<220>
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<400> 95

Ser Arg Pro Ser Gln Trp
1 5

<210> 96
<211> 6
<212> PRT
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<220>
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<400> 96

Thr Ser Glu Ala Asp His
1 5

<210> 97
<211> 6
<212> PRT
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<220>
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<400> 97

Thr Tyr Leu Asn Thr Pro
1 5

<210> 98

<211> 6
<212> PRT
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<220>
<223> Modified sequence of finger 2 of zif268

<400> 98

Gly Tyr Arg Ala Ala Pro
1 5

<210> 99
<211> 6
<212> PRT
<213> Artificial sequence

<220>
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<400> 99

Leu Tyr Arg Tyr His Leu
1 5

<210> 100
<211> 6
<212> PRT
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<220>
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<400> 100

Pro Thr Leu Val Asn Ala
1 5

<210> 101
<211> 6
<212> PRT
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<220>
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<400> 101

Val Arg Pro His Gln Arg
1 5

<210> 102
<211> 6
<212> PRT
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<220>

<223> Modified sequence of finger 2 of zif268

<400> 102

Pro Phe Cys Pro Tyr Arg
1 5

<210> 103

<211> 6

<212> PRT

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<220>

<223> Modified sequence of finger 2 of zif268

<400> 103

Gly Val Thr Met Gln Pro
1 5

<210> 104

<211> 6

<212> PRT

<213> Artificial sequence

<220>

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<400> 104

Pro Gln Pro Leu Ser Asp
1 5

<210> 105

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 2 of zif268

<400> 105

Arg Glu Gln Val Ser Arg
1 5

<210> 106

<211> 6

<212> PRT

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<220>

<223> Modified sequence of finger 2 of zif268

<400> 106

Thr His Met Trp Met Ile

1 5

<210> 107
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<220>
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<400> 107

Gln Arg Met Arg Thr Leu
1 5

<210> 108
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<212> PRT
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<220>
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<400> 108

Gln Arg Val Gly Leu Phe
1 5

<210> 109
<211> 6
<212> PRT
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<220>
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<400> 109

Leu Arg Thr Gly Asn Tyr
1 5

<210> 110
<211> 6
<212> PRT
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<220>
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<400> 110

Glu Arg Glu Phe Ser Leu
1 5

<210> 111
<211> 6

<212> PRT
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<400> 111

Glu Lys Glu Ser Arg Gly
1 5

<210> 112
<211> 6
<212> PRT
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<400> 112

Glu Gly Val Arg Lys Asn
1 5

<210> 113
<211> 6
<212> PRT
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<220>
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<400> 113

Thr Gly Val Asn Ser Ile
1 5

<210> 114
<211> 6
<212> PRT
<213> Artificial sequence

<220>
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<400> 114

Thr Gln Ala Arg Pro Pro
1 5

<210> 115
<211> 6
<212> PRT
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<220>
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<400> 115

Arg Asp Glu Arg Lys Arg
1 5

<210> 116

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 116

Arg Asp Leu Ala Asn Ser
1 5

<210> 117

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 117

Ser Gly Gln Trp Trp Arg
1 5

<210> 118

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 118

Ser Leu Leu Val Ile Ala
1 5

<210> 119

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 119

Val Ser Val Arg Gly Leu
1 5

<210> 120
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Modified sequence of finger 3 of zif268

<400> 120

Asn Val Gly Asp Lys Pro
1 5

<210> 121
<211> 6
<212> PRT
<213> Artificial sequence

<220>
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<400> 121

Ser Trp Ile Cys Gly Ile
1 5

<210> 122
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Modified sequence of finger 3 of zif268

<400> 122

Ile Ala Trp Met Glu Leu
1 5

<210> 123
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Modified sequence of finger 3 of zif268

<400> 123

Ile Met Met Thr Phe Phe
1 5

<210> 124
<211> 6
<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 124

Arg Glu Cys Arg Met Leu
1 5

<210> 125

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 125

Ile Ala Leu Leu Asp Thr
1 5

<210> 126

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Modified sequence of finger 3 of zif268

<400> 126

Asn Val Gln Gly Leu Arg
1 5

<210> 127

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved portion of Zif268 protein

<400> 127

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
1 5 10 15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
20 25 30

F9
cont